



001560-377.ST25.txt  
SEQUENCE LISTING

<110> SAKAKIBARA, Keiko  
FUKUI, Yuko  
TANAKA, Yoshikazu  
KUSUMI, Takaaki  
MIZUTANI, Masako  
NAKAYAMA, Toru

<120> GENE ENCODING PROTEIN HAVING AURONE SYNTHESIZING ACTIVITY

<130> 001560-377

<140> US 09/446,089

<141> 1999-12-17

<150> PCT/JP99/02045

<151> 1999-04-16

<150> JP 10/107296

<151> 1998-04-17

<160> 15

<170> PatentIn version 3.0

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<212> DNA

<213> Antirrhinum majus

<220>

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Met Phe Lys Asn Pro Asn  
1 5

atc cgc tat cac aaa cta tct tcc aaa tcc aat gac aac gat caa gaa 161  
Ile Arg Tyr His Lys Leu Ser Ser Lys Ser Asn Asp Asn Asp Gln Glu  
10 15 20

tcc tcc cat cgt tgt aag cac att cta tta ttt ata ata acc tta ttc 209  
Ser Ser His Arg Cys Lys His Ile Leu Leu Phe Ile Ile Thr Leu Phe  
25 30 35

cta ctt ata gtt ggc ctg tac atc gcc aac tct ctc gcc tat gcc cgg 257  
Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn Ser Leu Ala Tyr Ala Arg  
40 45 50

ttt gcc tcg acc tca acc ggc cct atc gcc gcc cct gat gtc acc aaa 305  
Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala Ala Pro Asp Val Thr Lys  
55 60 65 70

tgt ggt cag cca gac ttg cca cct ggc aca gcc cca ata aac tgt tgt 353  
Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr Ala Pro Ile Asn Cys Cys  
75 80 85

ccc cca atc ccc gct aaa atc atc gat ttc gag cta cca cct ccc tcc 401  
Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe Glu Leu Pro Pro Pro Ser  
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gat Asp 135	gac Asp	cct Pro	cgt Arg	agc Ser	ttc Phe 140	aag Lys	caa Gln	caa Gln	gct Ala	aac Asn 145	gtc Val	cat His	tgc Cys	gct Ala	tac Tyr 150	545
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ctc Leu	caa Gln 200	ttt Phe	tgg Trp	aac Asn	tat Tyr	gat Asp 205	tca Ser	cct Pro	ggt Gly	gga Gly	atg Met 210	aca Thr	atc Ile	cca Pro	tca Ser	737
atg Met 215	ttt Phe	att Ile	gat Asp	act Thr	aat Asn 220	tct Ser	tcg Ser	ctg Leu	tac Tyr	gat Asp 225	agt Ser	tta Leu	cgg Arg	gac Asp	agt Ser 230	785
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tcc Ser	gac Asp	aat Asn	acc Thr 250	act Thr	act Thr	cct Pro	gaa Glu	gag Glu 255	caa Gln	atg Met	att Ile	ata Ile	aac Asn 260	ctt Leu	aaa Lys	881
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aga Arg	gac Asp	ccg Pro	ata Ile 330	ttt Phe	ttt Phe	gct Ala	cat His 335	cat His	tcg Ser	aac Asn	gtc Val	gat Asp	aga Arg 340	atg Met	tgg Trp	1121
tcc Ser	ata Ile	tgg Trp 345	aag Lys	acc Thr	cta Leu	gga Gly	ggg Gly 350	ccg Pro	cgg Arg	agg Arg	acg Thr	gac Asp 355	tta Leu	aca Thr	gat Asp	1169
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 395 400 405

cca aaa gtt tct ccg tct cta ctt aag aaa ttt cat aga aca aac act 1361  
 Pro Lys Val Ser Pro Ser Leu Leu Lys Phe His Arg Thr Asn Thr  
 410 415 420

gcc aat ccg aga caa gtt ttt cct gcg ata ctt gac aga gtc tta aaa 1409  
 Ala Asn Pro Arg Gln Val Phe Pro Ala Ile Leu Asp Arg Val Leu Lys  
 425 430 435

gtt atc gtg acg agg ccg aag aaa act aga agt agg aaa gaa aag gac 1457  
 Val Ile Val Thr Arg Pro Lys Lys Thr Arg Ser Arg Lys Glu Lys Asp  
 440 445 450

gag tta gaa gag att tta gtg att gaa ggg att gaa ctg gaa aga gac 1505  
 Glu Leu Glu Glu Ile Leu Val Ile Glu Gly Ile Glu Leu Glu Arg Asp  
 455 460 465 470

cac ggg cac gta aaa ttc gac gtt tat att aat gct gac gaa gat gac 1553  
 His Gly His Val Lys Phe Asp Val Tyr Ile Asn Ala Asp Glu Asp Asp  
 475 480 485

ctt gcg gtg att tcg ccg gag aat gct gag ttc gcc ggg agt ttc gtg 1601  
 Leu Ala Val Ile Ser Pro Glu Asn Ala Glu Phe Ala Gly Ser Phe Val  
 490 495 500

agt ctg tgg cac aaa cct ata aag ggg aag agg aca aag acg cag tta 1649  
 Ser Leu Trp His Lys Pro Ile Lys Gly Lys Arg Thr Lys Thr Gln Leu  
 505 510 515

tta aca ttg tcg att tgt gat att ttg gag gat ttg gat gct gac gaa 1697  
 Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu Asp Leu Asp Ala Asp Glu  
 520 525 530

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 Asp Asp Tyr Val Leu Val Thr Leu Val Pro Arg Asn Ala Gly Asp Ala  
 535 540 545 550

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 Ile Lys Ile His Asn Val Lys Ile Glu Leu Asp Gly  
 555 560

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agcagttgta taaatggtga aataaggatt actttttgag 1951

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Phe Ile Ile Thr Leu Phe Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn  
 35 40 45  
 Ser Leu Ala Tyr Ala Arg Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala  
 50 55 60  
 Ala Pro Asp Val Thr Lys Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr  
 65 70 75 80  
 Ala Pro Ile Asn Cys Cys Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe  
 85 90 95  
 Glu Leu Pro Pro Pro Ser Thr Thr Met Arg Val Arg Arg Ala Ala His  
 100 105 110  
 Leu Val Asp Asp Ala Tyr Ile Ala Lys Phe Lys Lys Ala Val Glu Leu  
 115 120 125  
 Met Arg Ala Leu Pro Glu Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala  
 130 135 140  
 Asn Val His Cys Ala Tyr Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe  
 145 150 155 160  
 Thr Asn Leu Lys Leu Gln Ile His Arg Ser Trp Leu Phe Phe Pro Phe  
 165 170 175  
 His Arg Tyr Tyr Ile Tyr Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile  
 180 185 190  
 Asn Asp Thr Thr Phe Ala Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly  
 195 200 205  
 Gly Met Thr Ile Pro Ser Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr  
 210 215 220  
 Asp Ser Leu Arg Asp Ser Asn His Gln Pro Pro Thr Ile Val Asp Leu  
 225 230 235 240  
 Asn Tyr Ala Phe Ser Asp Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln  
 245 250 255  
 Met Ile Ile Asn Leu Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala  
 260 265 270  
 Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln  
 275 280 285  
 Glu Phe Pro Gly Val Gly Ser Ile Glu Leu Val Pro His Gly Met Ile  
 290 295 300

His Leu Trp Thr Gly Ser Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly  
 305 310 315 320  
 Ala Phe Tyr Ser Thr Ala Arg Asp Pro Ile Phe Phe Ala His His Ser  
 325 330 335  
 Asn Val Asp Arg Met Trp Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg  
 340 345 350  
 Arg Thr Asp Leu Thr Asp Pro Asp Phe Leu Asp Ala Ser Phe Val Phe  
 355 360 365  
 Tyr Asp Glu Asn Ala Glu Met Val Arg Val Lys Val Arg Asp Cys Leu  
 370 375 380  
 Asp Glu Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp  
 385 390 395 400  
 Leu Asn Thr Arg Pro Thr Pro Lys Val Ser Pro Ser Leu Leu Lys Lys  
 405 410 415  
 Phe His Arg Thr Asn Thr Ala Asn Pro Arg Gln Val Phe Pro Ala Ile  
 420 425 430  
 Leu Asp Arg Val Leu Lys Val Ile Val Thr Arg Pro Lys Lys Thr Arg  
 435 440 445  
 Ser Arg Lys Glu Lys Asp Glu Leu Glu Glu Ile Leu Val Ile Glu Gly  
 450 455 460  
 Ile Glu Leu Glu Arg Asp His Gly His Val Lys Phe Asp Val Tyr Ile  
 465 470 475 480  
 Asn Ala Asp Glu Asp Asp Leu Ala Val Ile Ser Pro Glu Asn Ala Glu  
 485 490 495  
 Phe Ala Gly Ser Phe Val Ser Leu Trp His Lys Pro Ile Lys Gly Lys  
 500 505 510  
 Arg Thr Lys Thr Gln Leu Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu  
 515 520 525  
 Asp Leu Asp Ala Asp Glu Asp Asp Tyr Val Leu Val Thr Leu Val Pro  
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 Arg Asn Ala Gly Asp Ala Ile Lys Ile His Asn Val Lys Ile Glu Leu  
 545 550 555 560  
 Asp Gly

<210> 3  
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<400> 3

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<210> 4  
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<210> 5  
 <211> 18  
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Glu Phe

<210> 6  
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 <221> UNSURE  
 <222> (8)..(8)  
 <223> Amino acid 8 is Xaa wherein Xaa = unknown or other.

<220>  
 <221> UNSURE  
 <222> (28)..(28)  
 <223> Amino acid 28 is Xaa wherein Xaa = unknown or other.

<400> 6

Lys Ile Ile Asp Phe Glu Leu Pro Xaa Pro Ser Thr Thr Met Arg Val  
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Arg Arg Ala Ala His Leu Val Asp Asp Ala Tyr Ile Xaa Lys  
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<210> 7  
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<400> 7

Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe Phe Gly Arg  
 Page 6

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 Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly Ser Ile Glu  
                   20                    25                    30  
 Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser Glu Asn Thr  
                   35                    40                    45  
 Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala Arg Asp Pro  
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 Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp Ser Ile Trp  
                   65                    70                    75                    80  
 Lys Thr Leu Gly Gly Pro Arg Arg Thr Asp Leu Thr Asp Pro Asp Phe  
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 Leu Asp Ala Ser Phe Val Phe Cys Asp Glu Asn Ala Glu Met Val Arg  
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 Val Lys Val Arg Asp Cys Leu Asp Gly Lys Lys Leu Gly  
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 <213> Artificial Sequence

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 <223> Primer

<220>  
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<210> 9  
 <211> 6  
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<220>  
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<220>  
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<210> 10  
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<220>

<223> Primer

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<210> 11

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<220>

<221> misc\_feature

<222> (6)..(18)

<223> Nucleotides 6, 15 and 18 are "n" wherein "n" = a or c or g  
or t/u or unknown or other

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20

<210> 12

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<220>

<221> misc\_feature

<222> (12)..(12)

<223> Nucleotide 12 is "n" wherein "n" = a or c or g or t/u  
or unknown or other

<400> 12

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17

<210> 13

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<220>

<221> misc\_feature

<222> (4)..(7)

<223> Nucleotides 4 and 7 are "n" wherein "n" = a or c or g or  
t/u or unknown or other

<400> 13

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18

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence



<220>

<223> Primer

<400> 14

aaggatccgg ccctatcgcc

20

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Primer

<400> 15

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22